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0590
211

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/003,671
Source: OPE
Date Processed by STIC: 12/12/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary .

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 101003,671

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☒ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering use space characters, instead.

- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 ☒ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☐ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/003,671

DATE: 12/12/2001

TIME: 14:13:00

Input Set : A:\36858Aseq.txt

Output Set: N:\CRF3\12112001\I003671.raw

Does Not Comply
Corrected Diskette Needed

Errors on pp. 1+2

4 <110> APPLICANT: Mize, Nancy K.
 5 Haley-Vicente, Dana A.
 8 <120> TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
 10 <130> FILE REFERENCE: 28110/36858A
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/003,671
 C--> 13 <141> CURRENT FILING DATE: 2001-11-02
 15 <150> PRIOR APPLICATION NUMBER: US 60/245,346
 16 <151> PRIOR FILING DATE: 2000-11-02
 19 <160> NUMBER OF SEQ ID NOS: 26
 22 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

706 <210> SEQ ID NO: 8
 708 <211> LENGTH: 177
 710 <212> TYPE: PRT
 712 <213> ORGANISM: Homo sapiens
 716 <400> SEQUENCE: 8
 718 Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
 720 1 5 10 15
 724 Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser
 726 20 25 30
 730 Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
 E--> 731 35 40 45
 735 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn
 737 50 55 60
 741 Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala
 743 65 70 75 80
 747 Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys
 749 85 90 95
 753 Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp
 755 100 105 110
 759 Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser
 761 115 120 125
 765 Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp
 767 130 135 140
 771 Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn
 773 145 150 155 160
 777 Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp
 779 165 170 175
 783 Glu

→ misalignment
 of amino acid
 numbering

- See error summ
 sheet item 3

1251 <210> SEQ ID NO: 19
 1252 <211> LENGTH: 26 → found 31
 1253 <212> TYPE: DNA
 1254 <213> ORGANISM: Artificial Sequence
 1256 <220> FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\36858Aseq.txt

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1257 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
1259 <400> SEQUENCE: 19
E--> 1260 gagccgccat gtgttcctc cccatggcaa g
1428 <210> SEQ ID NO: (2) → ? — discrepancy in numbering of sequence
1429 <211> LENGTH: (26) → found 37
1430 <212> TYPE: DNA
1431 <213> ORGANISM: Artificial Sequence
1433 <220> FEATURE:
1434 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
E--> 1436 <400> SEQUENCE: (26)
E--> 1437 gttttacttt gaacagagct ggtagtgatc aagcttc

(31)

length input
found 31

(37)

VERIFICATION SUMMARY

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Input Set : A:\36858Aseq.txt

Output Set: N:\CRF3\12112001\I003671.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:731 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:1260 M:252 E: No. of Seq. differs, <211>LENGTH:Input:26 Found:31 SEQ:19
L:1436 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:26
L:1437 M:252 E: No. of Seq. differs, <211>LENGTH:Input:26 Found:37 SEQ:2